Table 4: **p2p7p1p6**

HXB2 Location	Author Location	Sequence	Immunogen	Species(HLA)	References
p2p7p1p6(1–7)	Gag( )	VLAEAMSQV	HIV-1 infection	human(A*0201)	[Altfeld (2001d)]
• Epitope name: Gag-386. HIV was scanned for all peptides which carried the A2-supermotif pattern conserved in more than 50% of B clade sequences – 233 peptides met this criteria, and 30 of these bound to HLA-A*0201 – 20/30 bound to at least 3/5 of HLA-A2 supertype alleles tested • Three additional previously described HLA-A2 epitopes were added to the set of 20, and 18/22 chronically infected HLA-A2 individuals had CTL that recognized at least one of the 23 peptides (median of 2 and maximum of 6), while 6/12 acutely infected individuals recognized at least 1 (median of 1 and maximum of 2) • VLAEAMSQV binds to all five HLA-A2 supertype alleles tested: A*0201, A*0202, A*0203, A*0206 and A*6802 (highest affinity) • 4/22 individuals with chronic HIV-1 infection recognized this epitope, and it was immunodominant in 3/4 by ELISPOT • 0/12 acutely infected individuals recognized this epitope				
p2p7p1p6(1–7)	Gag(397–405)	VLAEAMSQV	HIV-1 infection	human(A2 supertype)	[Propato (2001)]
• Long-term nonprogressors (LTNPs) had strong memory resting CD8+ T-cell responses against the majority of epitopes tested (18 for the A2 supertype, 16 for the A3 supertype) while the effector cells of long-term nonprogressors recognized far fewer epitopes • Progressors had memory resting CD8+ T-cells that recognized far fewer epitopes than LTNPs • A positive correlation between effector CD8+ T-cells and plasma viremia and a negative correlation between CD8+ effector T-cells and CD4+ T-cells was observed, which may contribute to the inability of LTNPs to clear virus • This epitope can bind five HLA-A2 supertypes alleles (A*0201, A*0202, A*0203, A*0206 and A*6802)				
p2p7p1p6(5–13)	Gag( )	SQVTNPANI	Vaccine	murine BALB/c(H-2D^b)	[Paliard (1998)]
Vaccine: *Strain:* SF2 *HIV component:* Gag • HIV-1(SF2)p55gag vaccination of H-2 mice activates a CTL response against this epitope • CTL that recognized SQVTNPANI in the context of H-2D^b cross-reacted with H-2 alloantigens H-2L^d and an unidentified self-peptide • A postulate: heterozygosity at the MHC level could prevent the maturation of some T-cell receptor combinations for foreign peptide and self-MHC constructs because of thymic depletion and tolerance					
p2p7p1p6(18–37)	Gag( )	SNFKGNKRMVKCFNC-GKEGH		human(A*02011)	[Novitsky (2001)]
• This study provides a survey of CTL responses and full length HIV-1 genome sequences from a C subtype infected Botswanan cohort • 4/8 individuals (50%) who were positive for HLA-A*02011 responded to the peptide SNFKGNKRMVKCFNCGKEGH					
p2p7p1p6(55–70)	p15(446–460 BRU)	KEGHQMKDCTERQAN-F	HIV-1 infection	human(A2)	[Claverie (1988)]
• One of four epitopes first predicted, then subsequently shown to stimulate an HLA-A2 restricted CTL line					

p2p7p1p6(64–71)	Gag(427–434 HXB2)	TERQANFL	HIV-1 infection	human(B*4002)	[Mulligan (2001)]
	• Epitope G43 from Patient 07118 with HLA genotypes A*0209, A*3201, B*4002, B*5301, Cw*0202, Cw*0401 • Epitope G43 Patient 07118 has 4 more optimal peptides P55, PIQKETWETW with HLA A*3201; N10, KEKGGLEGL with HLA B*4002; G21 and G22, AEWDRVHPV with HLA B*4002;G31, QASQEVKNW with HLA B*5301				
p2p7p1p6(83–97)	p15(418–433 BRU)	GNFLQSRPEPTAPPF	HIV-1 infection	human(A2)	[Claverie (1988)]
	• One of four epitopes first predicted, then subsequently shown to stimulate an HLA-A2 restricted CTL line				
p2p7p1p6(118–126)	p2p7p1p6(118–126)	KELYPLTSL		human(B*4001(B60))	[Brander & Goulder(2001)]
	• C. Brander notes that this is a B*4001 epitope				
p2p7p1p6(121–130)	Gag(484–493)	YPLTSLRSLF	HIV-1 infection	human(B7)	[Jin (2000b)]
	• This B7 epitope is one of three subdominant CTL responses detected in a long-term non-progressor • A dominant B7 epitope was defined using conventional methods, and three additional sub-dominant HLA B7 epitopes were defined by first using a non-anchor based strategy, EpiMatrix, to identify 2078 possible epitopes in the autologous HIV-1, followed by B7 anchor residue prediction to narrow the set to 55 peptides for experimental testing				